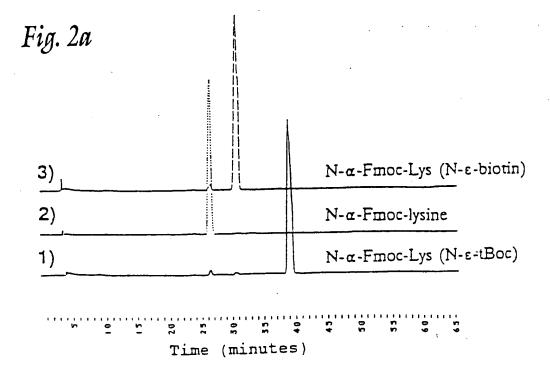
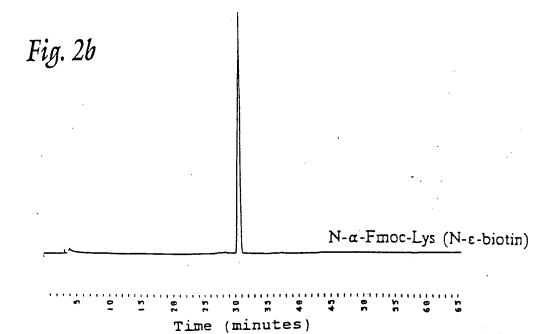
$$\begin{array}{c} CH_{3} \\ CH_{3} \\ CH_{4} \\ CH_{5} \\ CH_{2} \\ CH_{2} \\ CH_{2} \\ CH_{3} \\ CH_{4} \\ CH_{5} \\ CH_{5$$

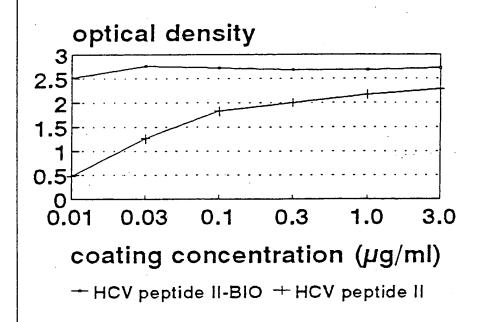
N-α-Fmoc-lysine (2) N-ck-Fmoc-Lys(N-E-tBoc) (1)

S

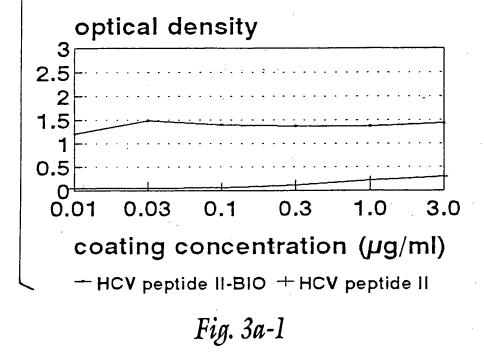
$$CH_2$$
 CH_2
 C







sample 8242



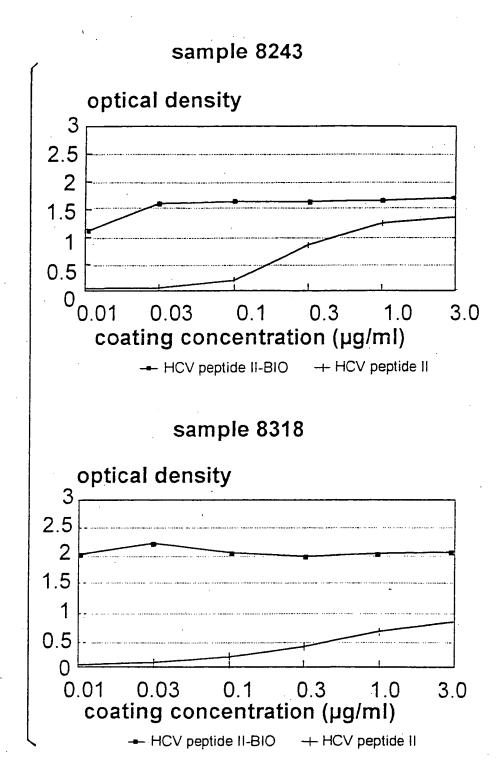
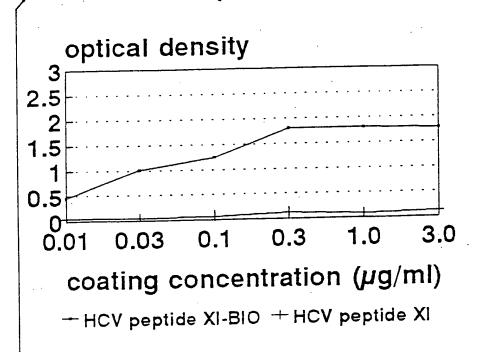


Fig. 3a-2



sample 8326

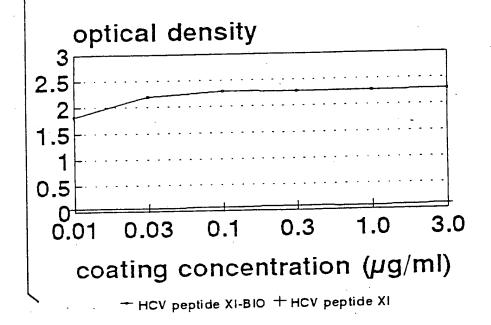


Fig. 3b-1

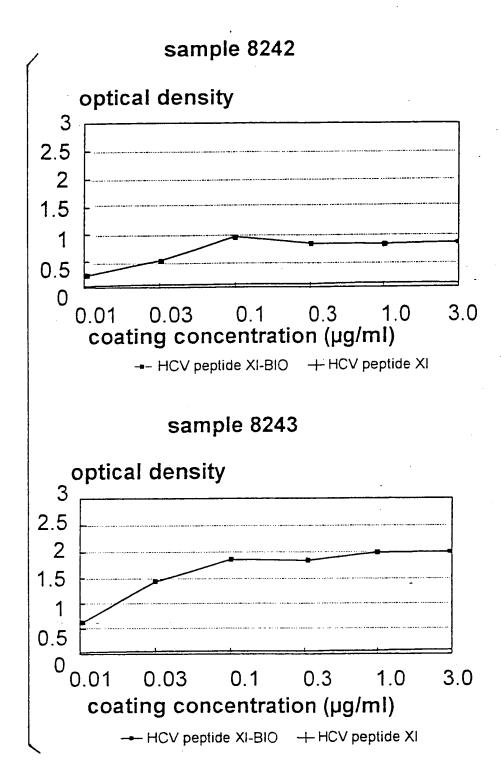
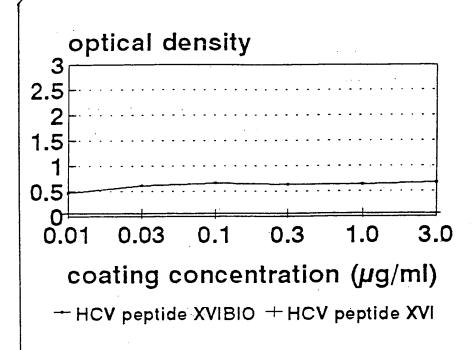


Fig. 3b-2



sample 8318

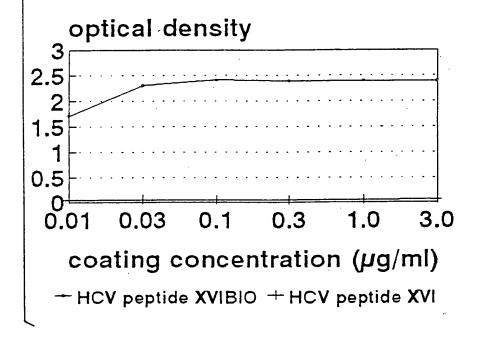


Fig. 3c-1

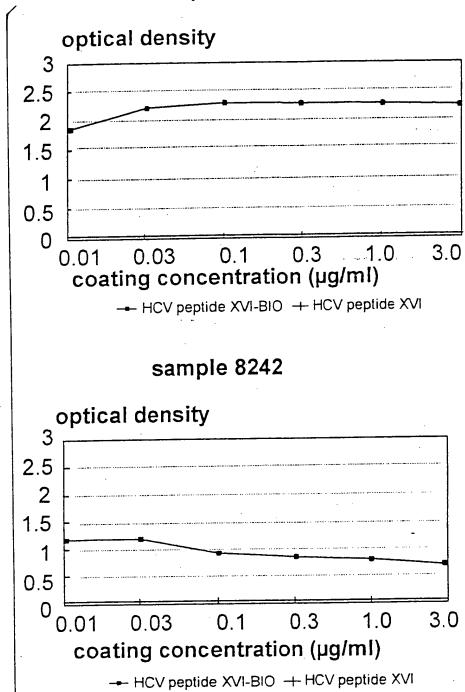
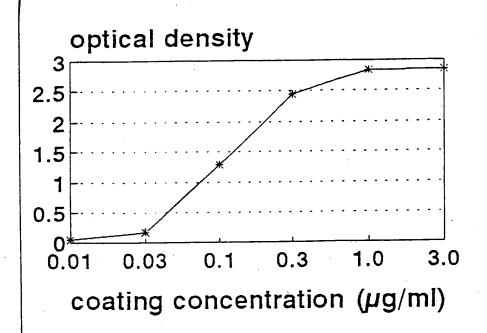
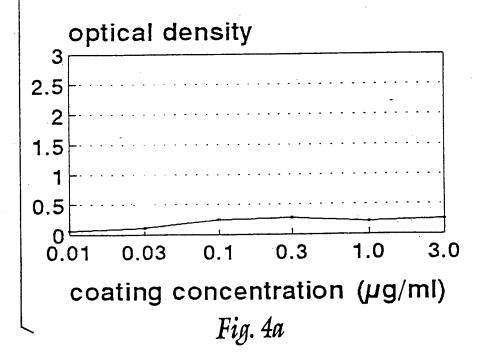


Fig. 3c-2

HCV peptide II-BIO



HCV peptide XI-BIO



HCV peptide XVI-BIO

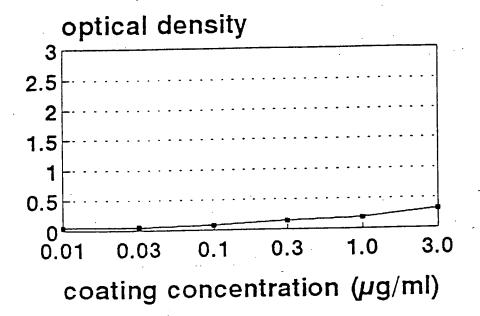
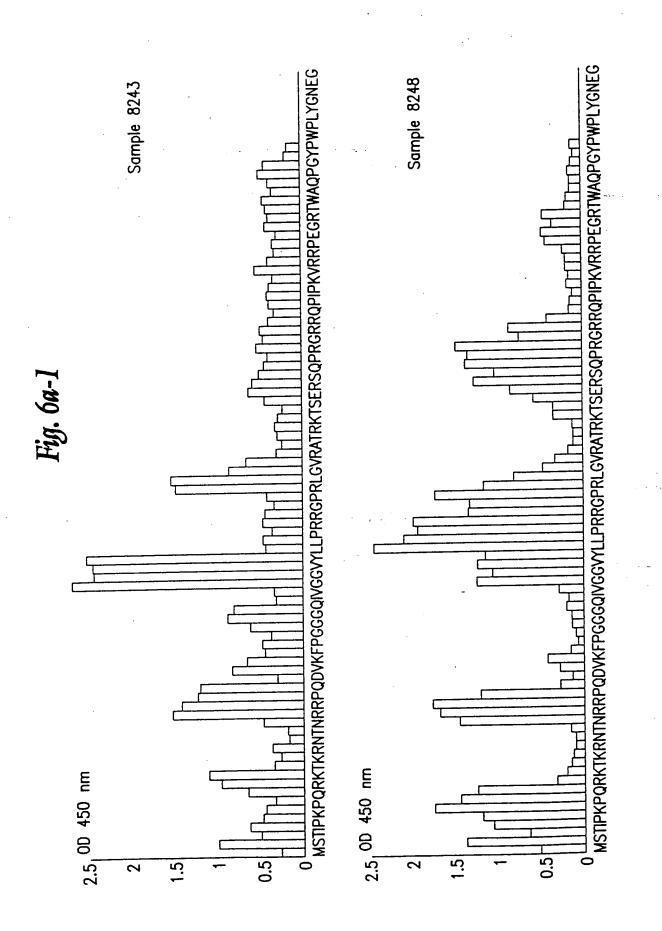
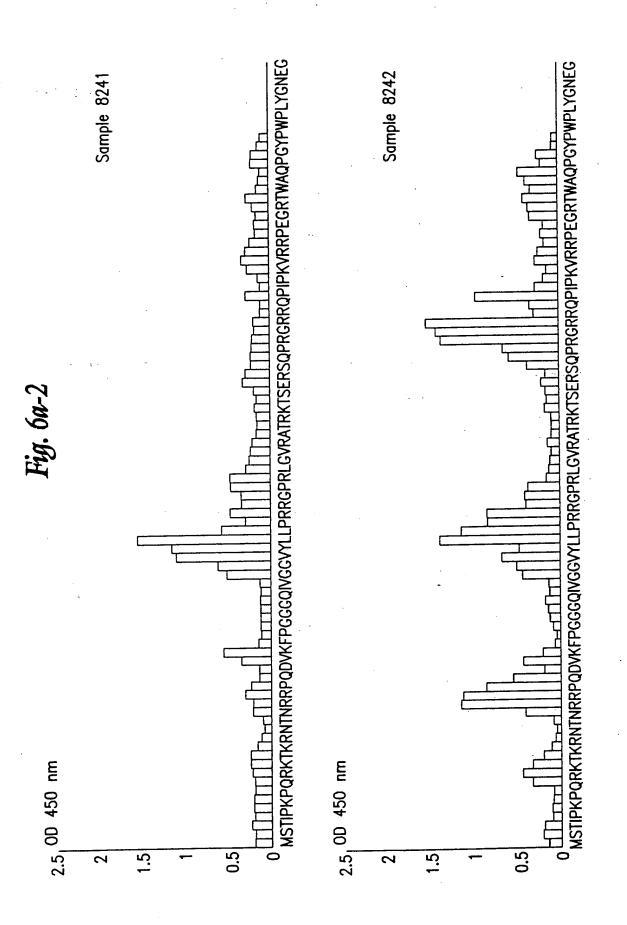


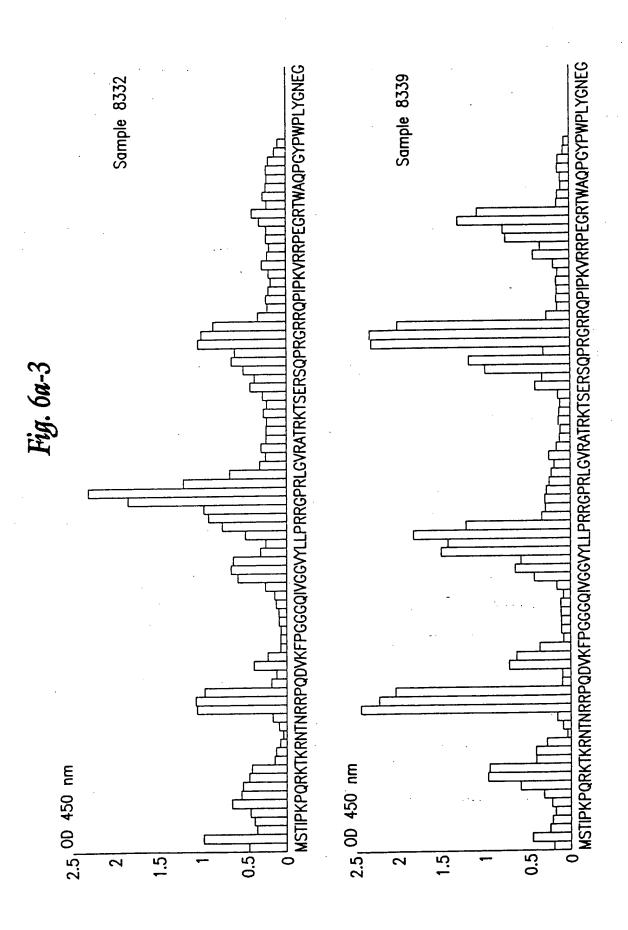
Fig. 4b

N-terminally biotinylated C-terminally TM peptide TM pe

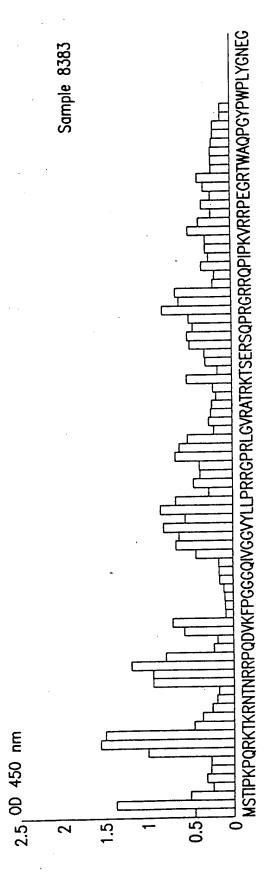
C-terminally biotinylated TM peptide

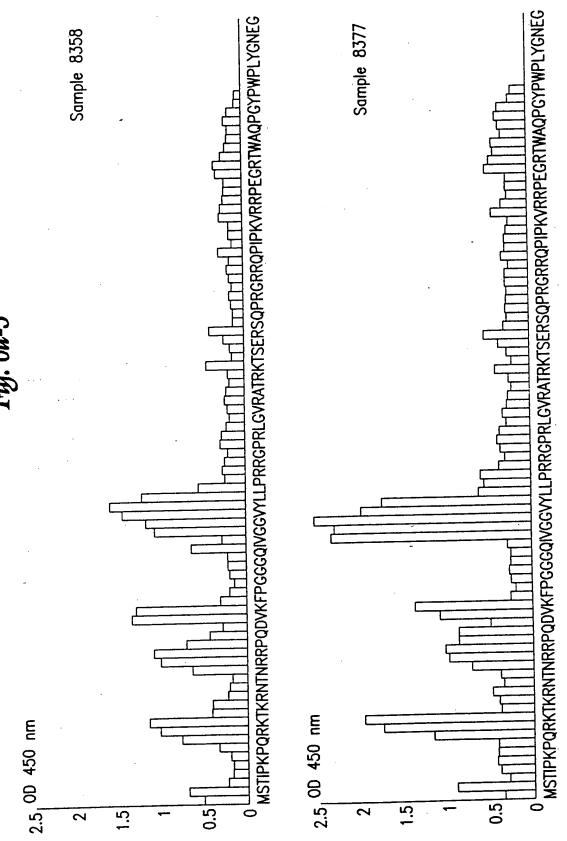


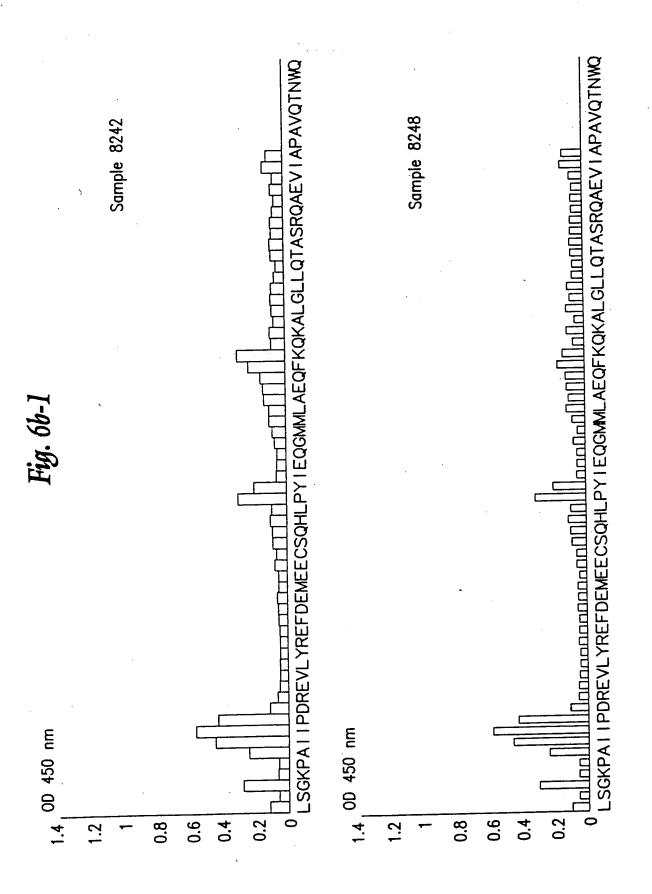


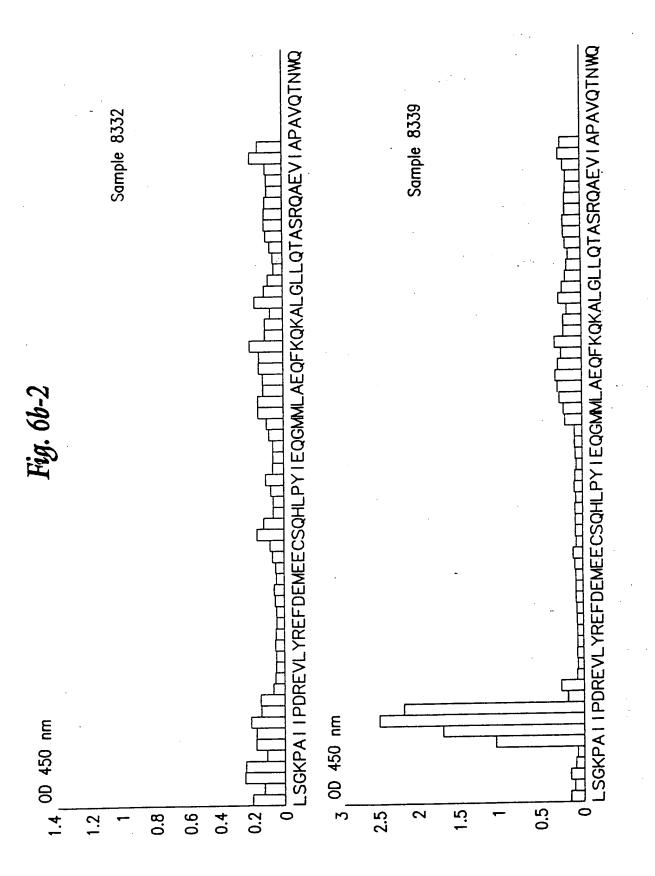


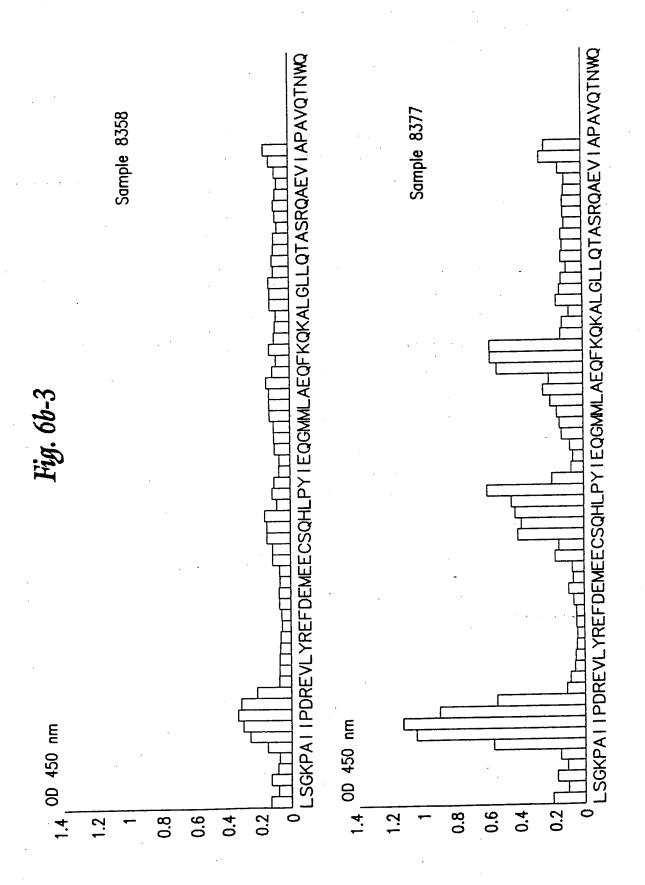
Sample 8378 Fig. 6a-4 2.5₁00 450 nm 0.5 5. 2

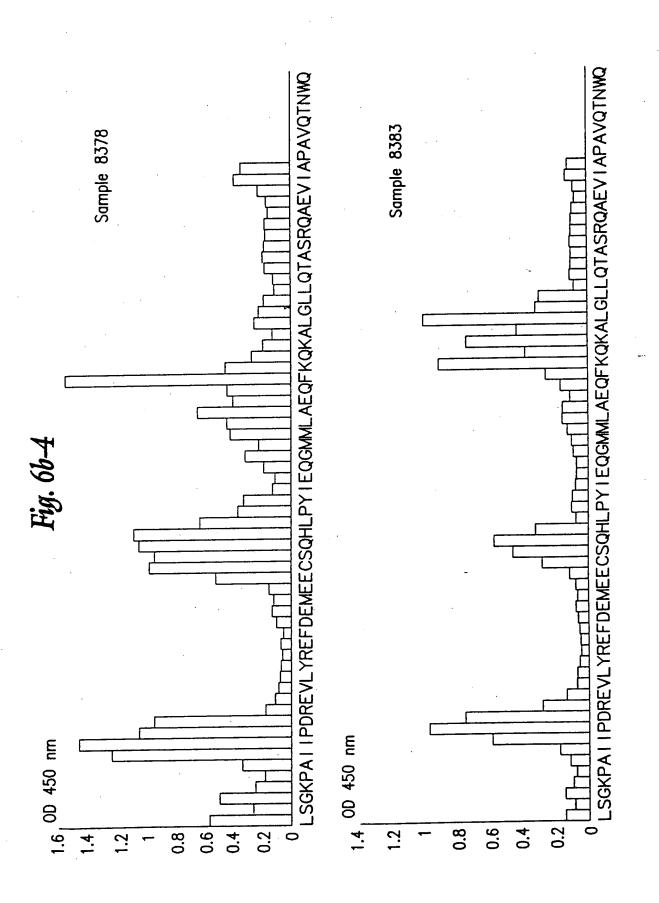


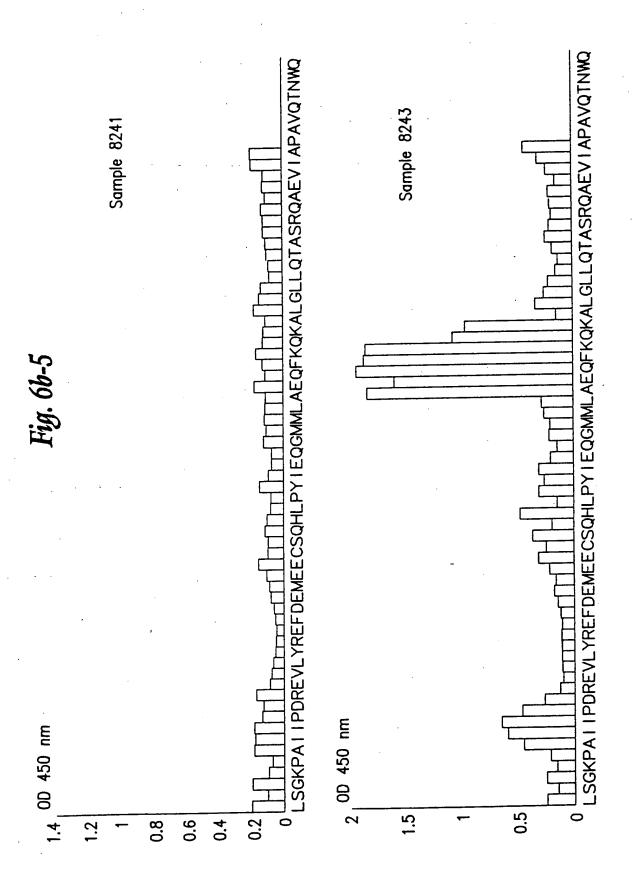


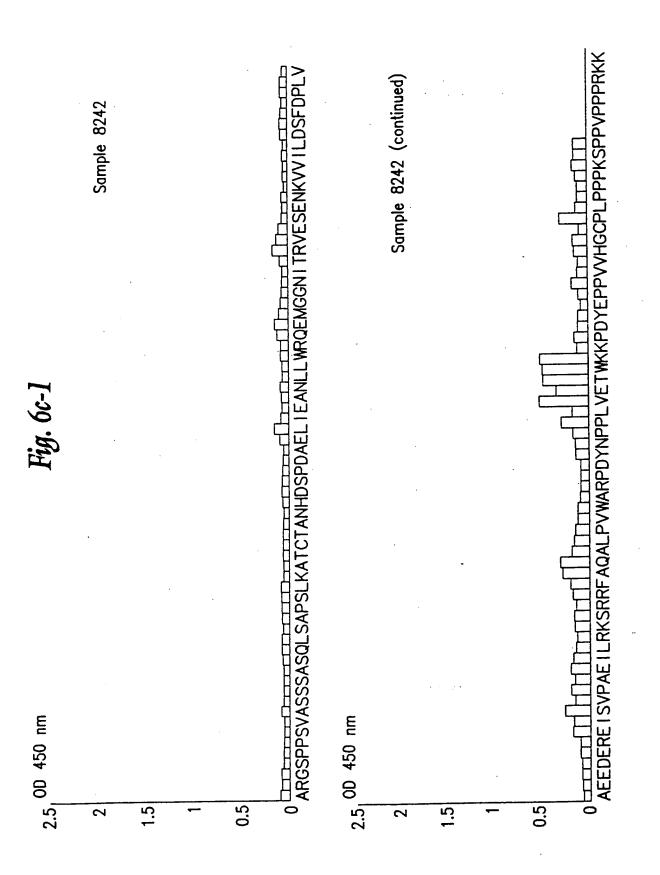


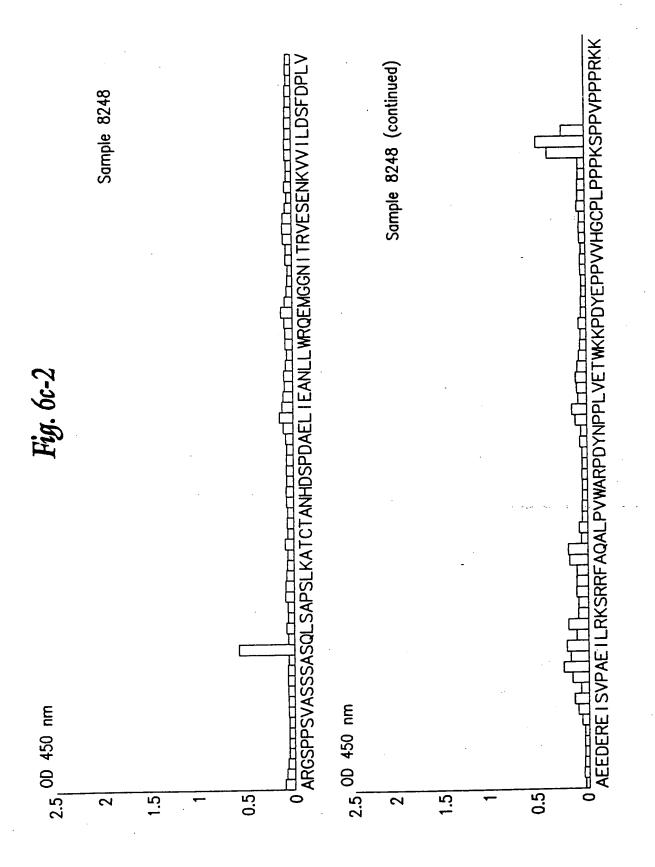


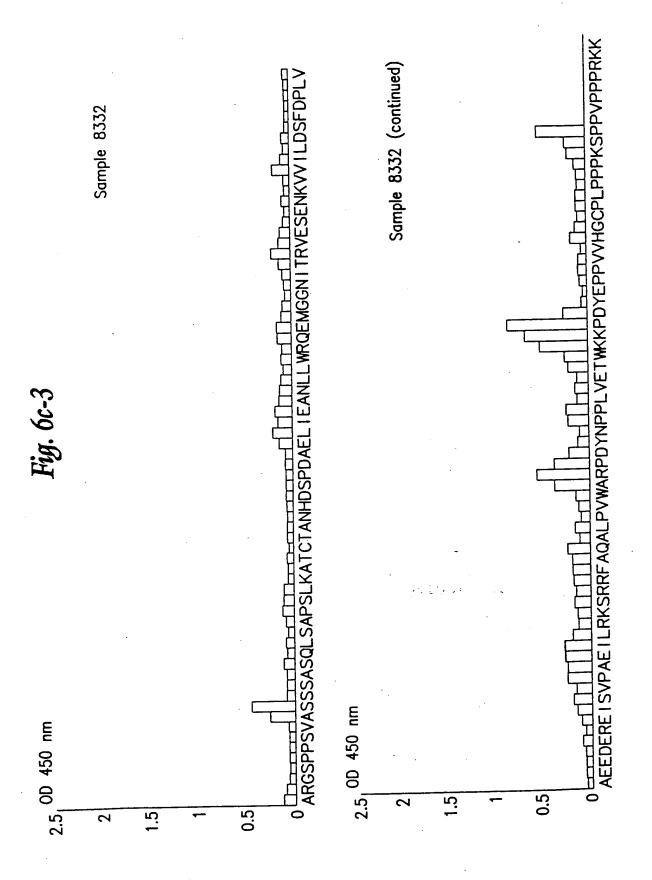


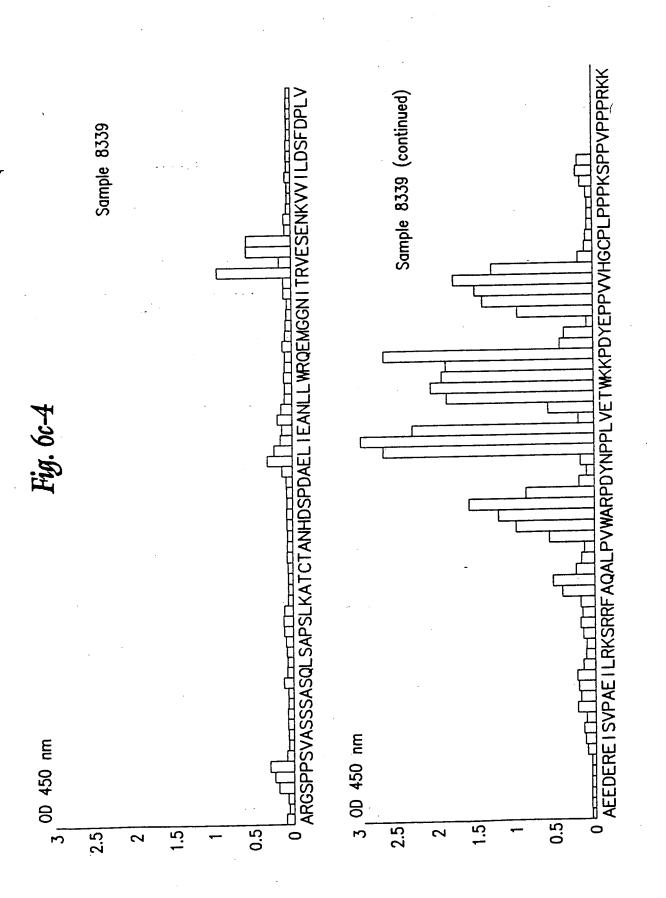


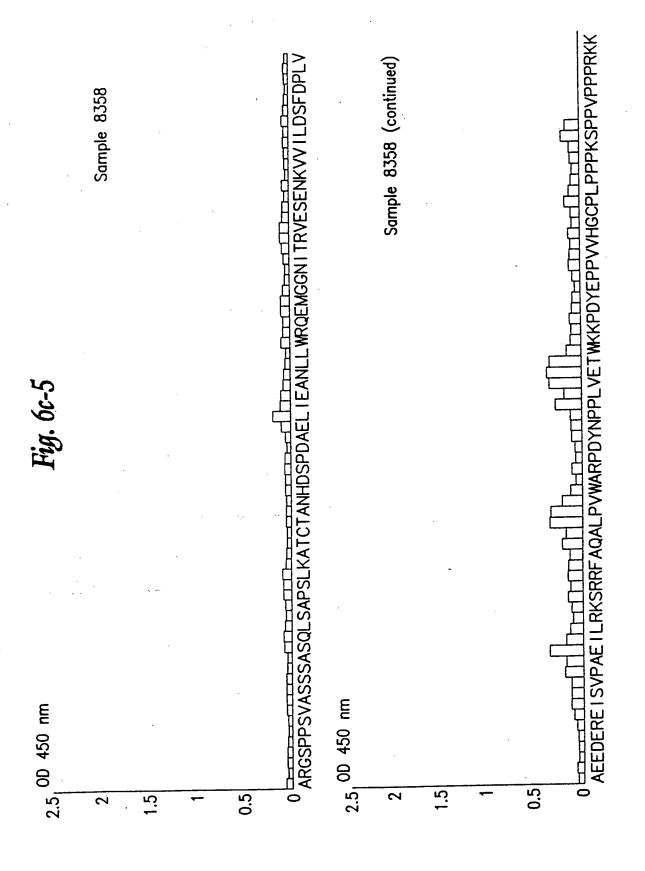


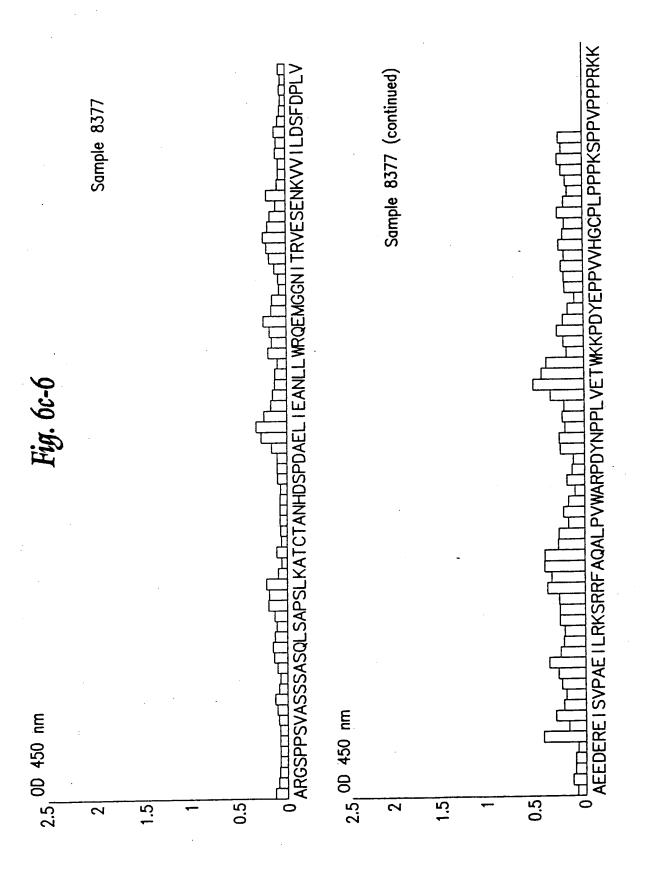


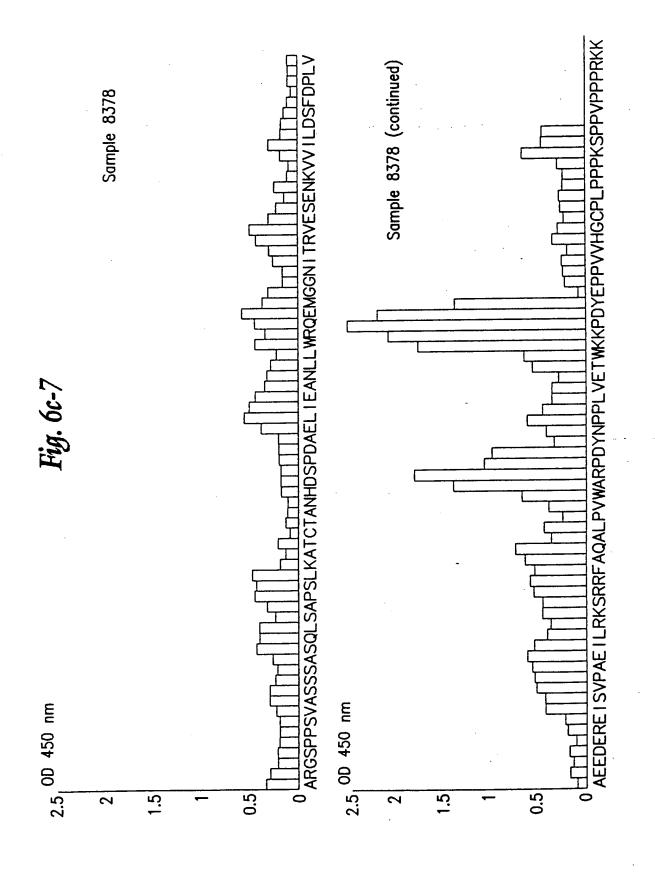


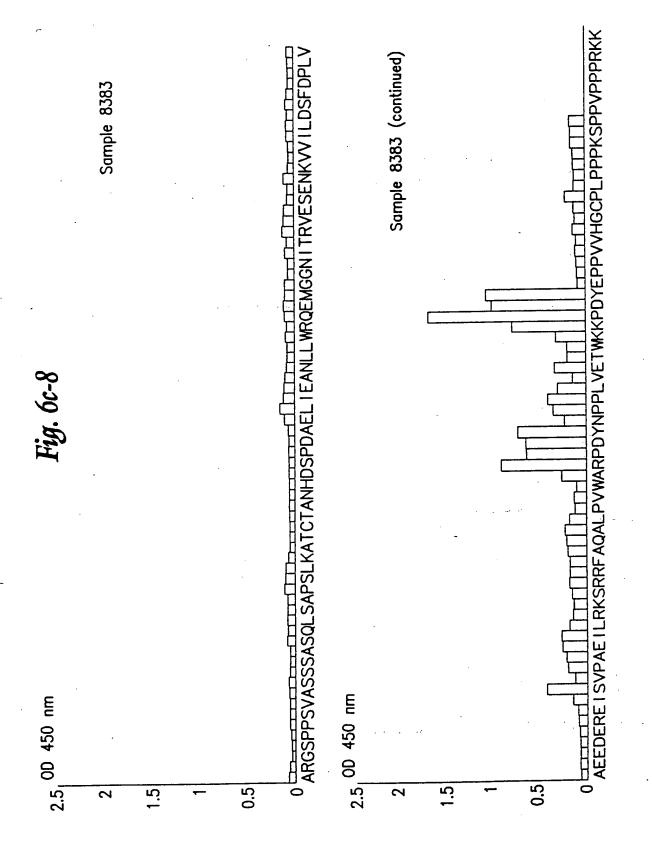


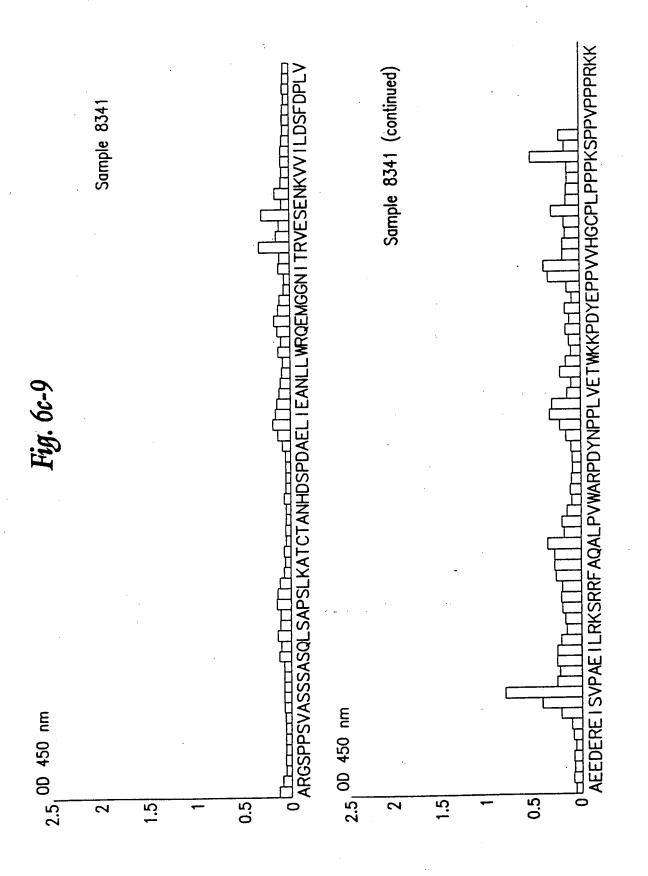












بيد تاه

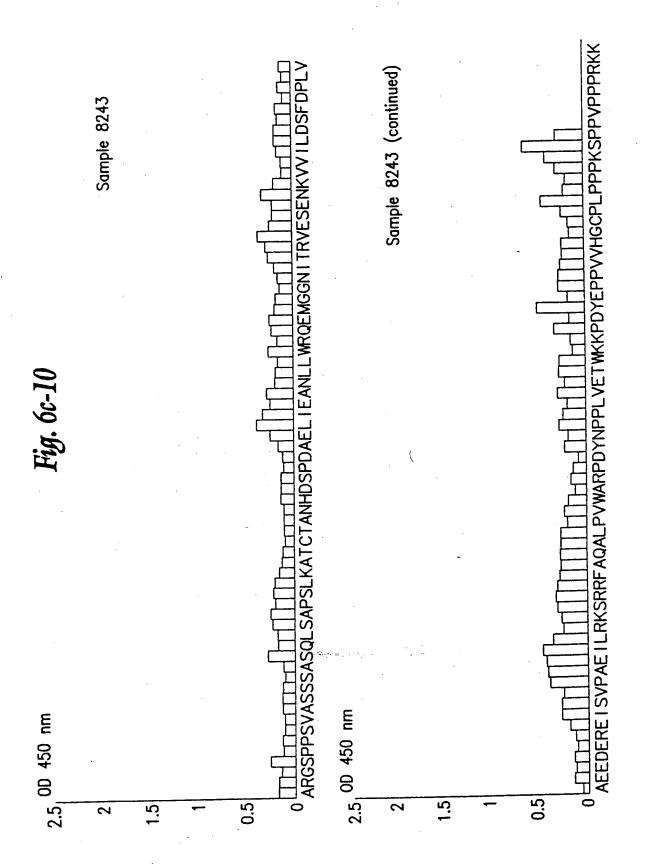


Fig. 7a-1

(SEQ ID NO:453)	(SEQ ID NO:454)	(SEQ ID NO:455)
MSTIPKPQRKTKRNTNRRPQ	PQRKTKRNTNRRPQDVKFPG	RNTNRRPQDVKFPGGGQIVG
\vdash	H	III
Peptide I	Peptide II	Peptide

	Peptide I		Peptide II		Peptide III
(SEQ ID NO:)	NO:)	(SEQ ID NO:)	NO:)	(SEQ ID NO:)	NO:)
(178)	MSTIPKPOR	(184)	PORKTKRNT	(190)	(190) RNTNRRPQD
(179)	STIPKPORK	(185)	QRKTKRNTN	(191)	NTNRRPQDV
(180)	TIPKPORKT	(186)	RKTKRNTNR	(192)	TNRRPQDVK
(181)	IPKPORKTK	(187)	KTKRNTNRR	(193)	NRRPQDVKF
(182)	PKPORKTKR	(188)	TKRNTNRRP	(194)	RRPQDVKFP
(183)	KPORKTKRN	(189)	KRNTNRRPQ	(195)	RPQDVKFPG
(187)	PORKTKRNT	(190)	RNTNRRPQD	(196)	PQDVKFPGG
(185)	ORKTKRNTN	(191)	NTNRRPQDV	(197)	QDVKFPGGG
(186)	RKTKRNTNR	(192)	TNRRPQDVK	(198)	DVKFPGGGQ
(187)	KTKRNTNRR	(193)	NRRPQDVKF	(199)	VKFPGGGQI
(101)	TKRNTNRRP	(194)	RRPQDVKFP	(200)	KFPGGGQIV
(189)	KRNTNRRPO	(195)	RPQDVKFPG	(201)	FPGGGQIVG

Fig. 7a-2

Core 5 Peptide IV Peptide V Peptide VI

PGGGQIVGGVYLLPRRGPRL (seq 1D NO:456)
LPRRGPRLGVRATRKTSERS (seq 1D NO:457)
(seq 1D NO:458) TRKTSERSQPRGRRQPIPKV

(SEQ ID NO:459) RRQPIPKVRRPEGRTWAQPG

Core 5		Peptide IV		Peptide V	ł	Peptides VI
(SEQ ID NO:)	(SEQ ID NO:)	NO:) (SEQ ID NO:)	D NO:)		(SEQ ID NO:)	NO:)
(202) PGGGQIVGG	(214)	LPRRGPRLG	(526)	TRKTSERSQ	(238)	RRQPIPKVR
(203) GGGQIVGGV	(215)	PRRGPRLGV	(227)	RKTSERSQP	(239)	RQPIPKVRR
(204) GGQIVGGVY	(216)	RRGPRLGVR	(228)	KTSERSQPR	(240)	QPIPKVRRP
(205) GQIVGGVYL	(217)	RGPRLGVRA	(229)	TSERSQPRG	(241)	PIPKVRRPE
(206) QIVGGVYLL	(218)	GPRLGVRAT	(230)	SERSQPRGR	(242)	IPKVRRPEG
(207) IVGGVYLLP	(219)	PRLGVRATR	(231)	ERSQPRGRR	(243)	PKVRRPEGR
(208) VGGVYLLPR	(220)	RLGVRATRK	(232)	RSQPRGRRQ	(544)	KVRRPEGRT
(209) GGVYLLPRR	(221)	LGVRATRKT	(233)	SQPRGRRQP	(245)	VRRPEGRTW
(210) GVYLLPRRG	(222)	GVRATRKTS	(234)	QPRGRRQPI	(546)	RRPEGRTWA
(211) VYLLPRRGP	(223)	VRATRKTSE	(235)	PRGRRQPIP	(247)	RPEGRTWAQ
(212) YLLPRRGPR	(224)	RATRKTSER	(536)	RGRRQPIPK	(248)	PEGRTWAQP
(213) LLPRRGPRL	(225)	ATRKTSERS	(237)	GRRQPIPKV	(548)	EGRTWAQPG

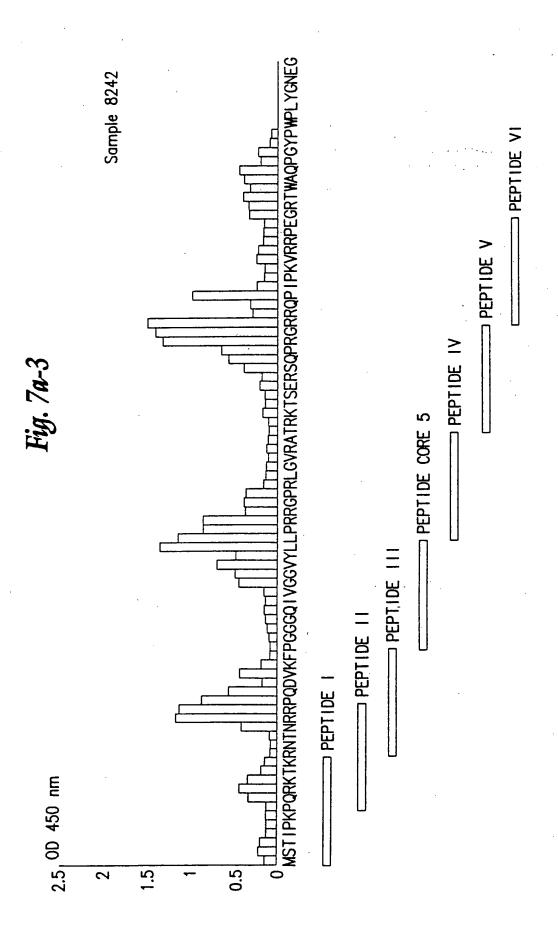


Fig. 7b-1

LSGKPAIIPDREVLYREFDE (SEQ ID NO: 460)	IIPDREVLYREFDEMEECSQ (seq id no:460)	VLYREFDEMEECSQHLPYIE (seq 1D NO:462)	DEMEECSQHLPYIEQGMMLA (seq 1D NO:463)	SQHLPYIEQGMMLAEQFKQK (seq 1D NO:464)	I EQGMMLAEQFKQKALGLLQ (SEQ ID NO:465)	
HCV1	HCV2	HCV3	HCV4	HCV5	9ЛЭН	

HCV6	(SEQ ID NO:) Q 288IEQGMMLAE	EQGMMLAEQ	QGMMLAEQF	GMMLAEOFK	MMLAEQFKO	MLAEQFKQK	LAEQFKQKA	AEQFKQKAL	EQFKQKALG	QFKQKALGL	FKQKALGLL	KQKALGLLQ
75	10:) (SEQ 1LPYIEQ 288	PYIEQG 289	$ m YIEQGM_{290}$	CIEQGMM 291	EQGMML 292	EQGMMLA 293	CHMLAE 294	SMMLAEQ 295	IMLAEQF 296	ILAEQFK 297	AEQFKQ 298	LEQFKQK 299
HCV5	(SEQ ID NO:) CSQH 282SQHLE	SQHL 283QHI	QHLP 284HLE	HLPY 285LP3	LPYI 286PY1	PYIE 287YII	YIEQ 288 IEC	TEQG 289EQC	EQGM 290QGN	QGMM 291GMN	GMML 292MMI	MMLA 293MLP
HCV4	(SEQ ID NO:) EM276 DEMEE	ME277 EMEEC	EE278 MEECS	EC279 EECSQ	CS ₂₈₀ ECSQH	SQ281 CSQHL	2H282 SQHLP	HL283 QHLPY	LP284 HLPYI	PY285 LPYIE	YI 286 PYIEQ	IE287 YIEQG
HCV3	(SEQ ID NO:) 270VLYREFD	LYR 271LYREFDEME277 EMEECSQHL 283QHLPYIEQG 289EQGMMLAEQ	272YREFDEM	273REFDEME	GFD 274EFDEMEECS 280 ECSQHLPYI 286PYIEQGMML 292MMLAEQFKQ	275FDEMEEC:	DEM 276DEMEECSQH282 SQHLPYIEQ 288 I EQGMMLAE 294LAEQFKQKA	277EMEECSQI	278MEECSQH	EEC 279EECSQHLPY 285 LPYIEQGMM 291GMMLAEQFK 297QFKQKALGL	ECS 280ECSQHLPYI286 PYIEQGMML 292MMLAEQFKQ 298FKQKALGLL	281CSQHLPY
HCV2	(SEQ ID NO:) (SEQ	265I PDREVLYR	(260) GKPAIIPDR 266PDREVLYRE 272YREFDEMEE 278 MEECSQHLP 284HLPYIEQGM 290QGMMLAEQF	(261) KPAIIPDRE 26 DREVLYREF 273REFDEMEEC 279 EECSQHLPY 285LPYIEQGMM 291GMMLAEQFK	268 REVLYREFD	(263) AIIPDREVL269 EVLYREFDE 275FDEMEECSQ281 CSQHLPYIE 287YIEQGMMLA 293MLAEQFKQK	270 VLYREFDEM	(265) IPDREVLYR271 LYREFDEME 277EMEECSQHL283 QHLPYIEQG 289EQGMMLAEQ 295AEQFKQKAL	(266) PDREVLYRE ²⁷² YREFDEMEE 278MEECSQHLP ²⁸⁴ HLPYIEQGM 290QGMMLAEQF 296EQFKQKALG	273 REFDEMEEC	274 EFDEMEECS	(269) EVLYREFDE 275 FDEMEECSQ 281CSQHLPYIE287 YIEQGMMLA 293MLAEQFKQK 299KQKALGLLQ
HCV1	(SEQ ID NO:) (258) LSGKPAIIP	(259) SGKPAIIPD 265IPDREVI	GKPAIIPDR	KPALIPDRE	(262) PAIIPDREV ₂₆₈ REVLYRI	AIIPDREVL	(264) IIPDREVLY270 VLYREFI	IPDREVLYR	PDREVLYRE	(267) DREVLYREF ²⁷³ REFDEMI	(268) REVLYREFD274 EFDEMEI	EVLYREFDE
	(SEQ (258)	(259)	(260)	(261)	(262)	(263)	(264)	(265)	(366)	(267)	(268)	(568)

Fig. 76-2

LAEQFKQKALGLLQTASRQA (SEQ ID NO:466)	QKALGLLQTASRQAEVIAPA (SEO ID NO:467)	LQTASRQAEVIAPAVQTNWO (SEQ 1D NO:468)
HCV7	HCV8	HCV9

HCV9
HCV8
HCV7

(SEQ ID NO:)	QKALGLLQT (306) LQTASRQAE	LA (307) QTASRQAEV	AS (308) TASRQAEVI	SR (309) ASRQAEVIA	RQ (310) SRQAEVIAP	ON (311) ROAEVIAPA	AE (312) QAEVIAPAV	3V (313) AEVIAPAVQ	/I (314) EVIAPAVQT	[A (315) VIAPAVQTN	AP (316) IAPAVQTNW	CMINITOLING (FIE) AC
) NO:)	OKALGLLC	KALGLLQTA (307)	ALGLLQTAS (308)	LGLLQTASR	GLLQTASRQ (310)	LLQTASRQA (311)	LQTASRQAE (312)	QTASRQAEV (313)	TASRQAEVI	ASRÓAEVIA	SRQAEVIAP	CIC KONTURNOO
(SEQ ID NO:)	KQKA (300)	2KAL (301)	(ALG (302)	ALGL (303)	JGLL (304)	3LLQ (305)	LLQT (306)	LQTA (307)	ZTAS (308)	FASR (309)	ASRQ (310)	(111) עטמב
(SEQ ID NO:)	(294) LAEQFKQKA (300)	(295) AEQFKQKAL (301)	(296) EQFKQKALG (302)	(297) QFKQKALGL (303)	(298) FKQKALGLL (304)	(299) KQKALGLLQ (305)	(300) QKALGLLQT (306)	(301) KALGLLQTA (307)	(302) ALGLLQTAS (308)	(303) LGLLQTASR (309)	(304) GLLQTASRQ (310)	(311) (311)

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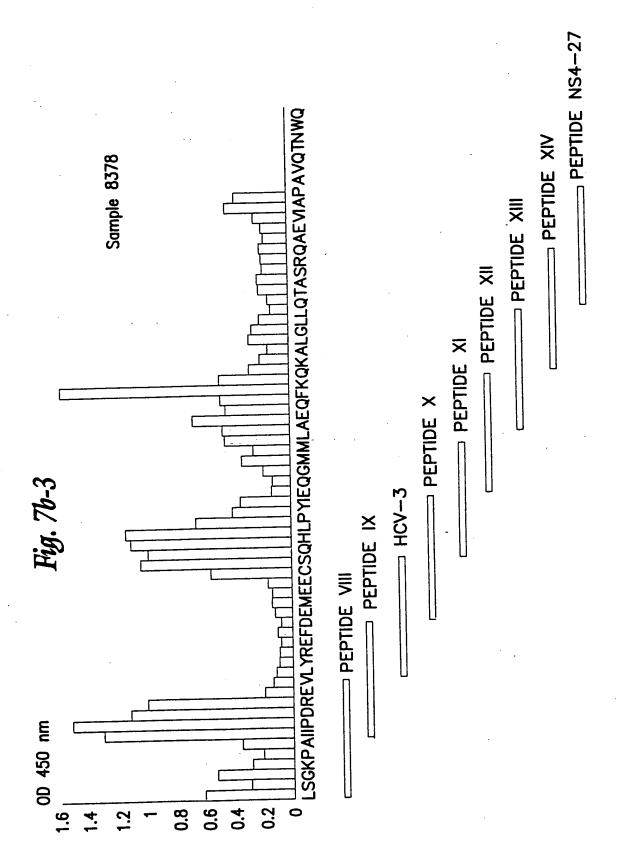


Fig. 7c-1

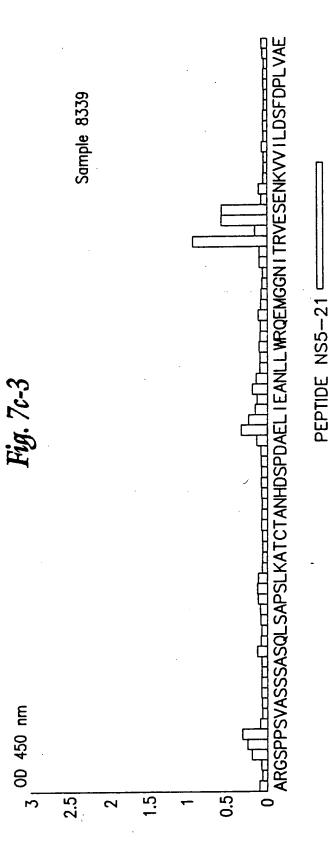
GNITRYESENKVVILDSFDP (seq 1D NO:469)	VILDSFDPLVAEEDEREISV (seq id no:470)	EDEREISVPAEILRKSRRFA (seq 1D NO:471)	(SEQ ID NO:472) LRKSRRFAQALPVWARPDYN	(SEQ ID NO:473) VWARPDYNPPLVETWKKPDY
NS5-21	NS5-23	NS5-25	NS5-27	NS5-29

NS5-29	SEQ ID NO: 318 GNITRYESE 330VILDSFDPL 342 EDEREISVP 354LRKSRRFAQ366 VWARPDYNP	NITRYESEN 331ILDSFDPLV 343DEREISVPA 355RKSRRFAQA367 WARPDYNPP	ITRYESENK 332LDSFDPLVA 344 EREISVPAE 356KSRRFAQAL 368 ARPDYNPPL	TRYESENKV $_{333}$ DSFDPLVAE $_{345}$ REISVPAEI $_{357}$ SRRFAQALP $_{369}$ RPDYNPPLV	RYESENKVV 334SFDPLVAEE 346EISVPAEIL 358RRFAQALPV 370 PDYNPPLVE	YESENKVVI335 FDPLVAEED 347 I SVPAEILR 359RFAQALPVW371 DYNPPLVET	ESENKVVIL1336 DPLVAEEDE 348SVPAEILRK 360FAQALPVWA 372 YNPPLVETW	SENKVVILD337 PLVAEEDER 349VPAEILRKS 361AQALPVWAR 373NPPLVETWK	ENKVVILDS338 LVAEEDERE 350PAEILRKSR 362QALPVWARP 374 PPLVETWKK	NKVVILDSF339 VAEEDEREI 351AEILRKSRR 363ALPVWARPD 375 PLVETWKKP	KVVILDSFD340 AEEDEREIS 352EILRKSRRF 364LPVWARPDY 376LVETWKKPD	VVILDSFDP341 EEDEREISV 353ILRKSRRFA 365PVWARPDYN 377VETWKKPDY
NS5-27	SEQ ID NO: 354LRKSRRFP	355RKSRRFAC	356KSRRFAQP	357SRRFAQAL	358RRFAQALE	359RFAQALPV	360FAQALPVW	361AQALPVWP	362QALPVWAF	363ALPVWARE	364LPVWARPL	365PVWARPDY
NS5-25	SEQ ID NO:	343 DEREI SVPA	. 344 EREISVPAE	345REISVPAEI	346EISVPAEIL	347 I SVPAEILR	348SVPAEILRK	. 349VPAEILRKS	350PAEILRKSR	351AEILRKSRR	352EILRKSRRF	353ILRKSRRFA
NS5-23	SEQ ID NO: 330VILDSFDPL	331ILDSFDPLV	332LDSFDPLVA	333DSFDPLVAE	334SFDPLVAEE	335 FDPLVAEED	336 DPLVAEEDE	1337 PLVAEEDER	338 LVAEEDERE	339 VAEEDEREI	340 AEEDEREIS	341 EEDEREISV
NS5-21	ONITRYESE	NITRYESEN	ITRYESENK	TRYESENKV	RYESENKVV	YESENKVVI	ESENKVVIL	SENKAVILD	ENKVVILDS	NKVVILDSF	KVVILDSFD	
	SEQ 11	319	320	321	322	323	324	325	326	327	328	329

Fig. 7c-2

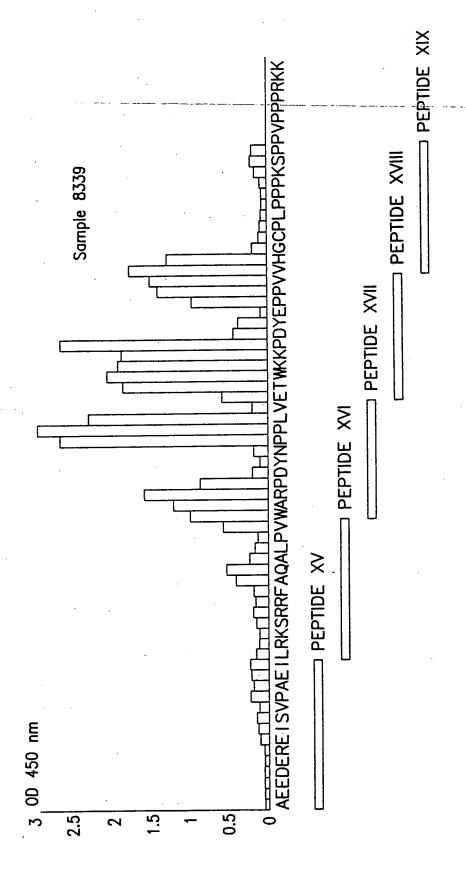
ETWKKPDYEPPVVHGCPLPP (seq 1D NO:474) (SEQ 1D NO:475) VHGCPLPPPKSPPVPPRKK NS5-33 NS5-31

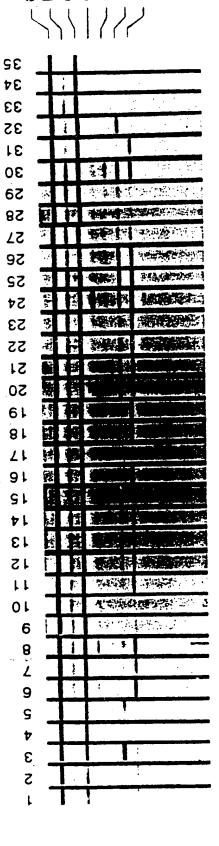
GCPLPPKSP PKSPPVPPP VHGCPLPPK HGCPLPPKS CPLPPKSPP PPKSPPVPP KSPPVPPPR SPPVPPPRK PPPKSPPVP PLPPKSPPV PPVPPPRKK LPPPKSPPV NS5-33 (SEQ ID NO:) 398 397 ETWKKPDYE EPPVVHGCP, PPVVHGCPL TWKKPDYEP WKKPDYEPP KKPDYEPPV PDYEPPVVH DYEPPVVHG YEPPVVHGC **PVVHGCPLP** VVHGCPLPP KPDYEPPVV NS5-31 (SEQ ID NO:) 387 383 384 385 381 382



PEPTIDE NS5-23 c

Fig. 7c-4





a: High intensity control b: Low intensity control

Peptide XXg-1, unbiotinylated c: Medium intensity control

e: Peptide XXg-2, unbiotinylated

g: Biotinylated peptide XXg-2: streptavidin complex f: Biotinylated peptide XXg-1: streptavidin complex

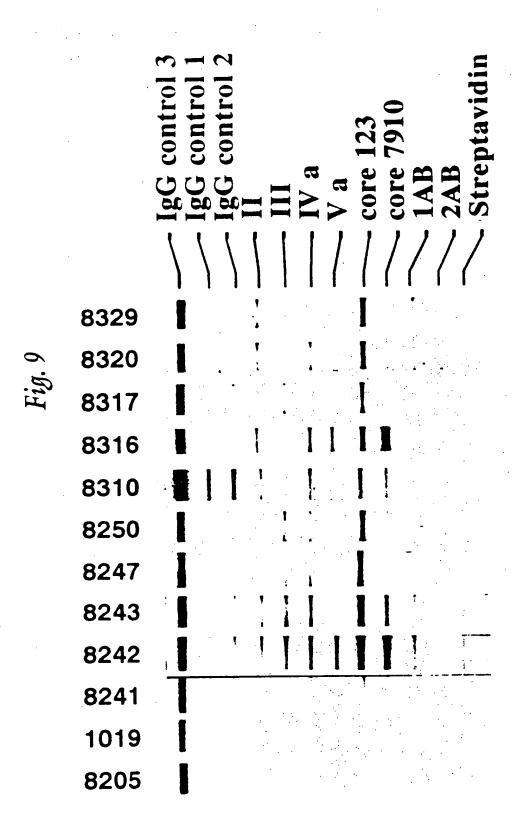


Fig. 10

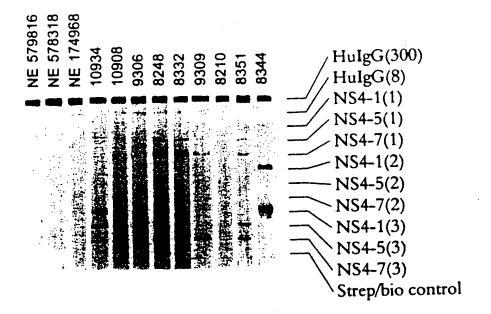


Fig. 11

/

Peptide	Sequence
NS4-a	GALVAFKIMSGEVPSTEDLV (SEQ ID NO:445)
NS4-b	VPSTEDLVNLLPAILSPGAL (SEQ ID NO:446)
NS4-c	AILSPGALVVGVVCAAILRR (SEQ ID NO:447)
NS4-d	(SEQ ID NO:448) VCAAILRRHVGPGEGAVQWM
NS4-e	(SEQ ID NO:449) GEGAVQWMNRLIAFASRGNH

Fig. 12

(SEQ ID NO:)	
Peptide	Amino Acid Sequence
Epi-152	Bio- GG-, IPDREVLYRGGKKPDYEPPVGGRRPQDVKFP
(450)	NS4 NS5 Core epitope 2
Epi-33B3A	Bio-GG-WARPDYNPPGGQFKQKALGLGSGVYLLPRRG
(451)	NS5 NS4 Core epitope 3 epitope 38
Epi-4B2A6	Bio-GG-RGRROPIPKGGSQHLPYIEQSGPVVHGCPLP
(452)	Core NS4 NS5 epitope 4B epitope 2A epitope 6

...

			280		control	carbonate buffer		control	
	IgG control 3	IgG control 1 IgG control 2	Epi - 152	Epi - 4B2A6	idin		Epi - 4B2A6	Streptavidin	
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Fig. 14a			Fia. 14b	0													•			
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23	Q G C A A A A A A A A A A A A A A A A A A	RAMSGLVSLFTPGAKQNIQLINT																		
		Partial sequence PEPTIDE XXg	2	4	16	64	192	768	4608	9216	46080	138240	414720	1658880	6635520	59719680	238878720	1911029760	1.1466179 E 10	No. of Variants

Fig. 14c

9	48	192	1728	6912	27648	82944	248832	1244160	2488320	14929920	59719680	179159040	716636160	2866544640	5733089280	1.1466179 E 10	No. of Variants

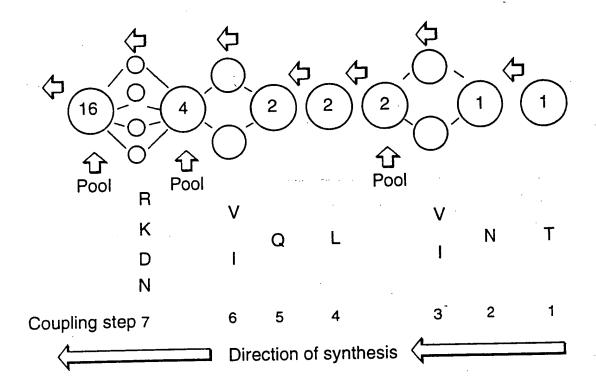
Section 1

Fig. 14d

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27648 13824	5184	6480	1440	2160	2160	720	720	576	288	192	96	96	32	16	16	4	No. of Variants

Fig. 15

Mixotope Synthesis Strategy



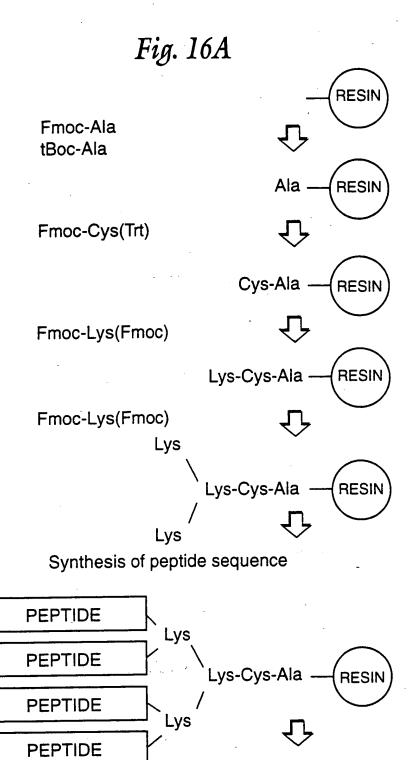
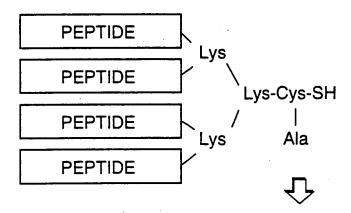
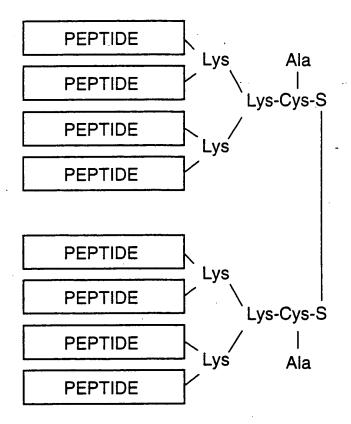


Fig. 16B

Cleavage and side-chain deprotection



Oxidation and dimerization



RABBIT 325, 326: XXb-2-MAP RABBIT 327, 328: XXg-2-MAP

